

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 4, 2002, 12:20:59 : Search time 21 Seconds
(Without alignments)
2512.050 Million cell updates/sec

Title: US-09-972-268-6

Perfect score: 349
Sequence: 1 MARRLEPSPLCGSGKAGLS.....EDLVSHVDSVISREMYV 549

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Cal number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database : 1
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	332	58.7	407	2	T08732
2	106	1.5	106	2	H71133
3	106	1.5	106	2	T06479
4	132	1.5	132	2	A55410
5	266	1.5	266	2	G83178
6	293	1.5	293	2	S47094
7	341	1.5	341	2	C83578
8	342	1.5	342	2	T45456
9	342	1.5	342	2	JC7110
10	452	1.5	452	2	T29618
11	459	1.5	459	1	KCHUI
12	470	1.5	470	2	AB1804
13	470	1.5	470	2	AD1430
14	503	1.5	503	2	B81690
15	503	1.5	503	2	C71535
16	513	1.5	513	2	D88991
17	594	1.5	594	2	I56248
18	594	1.5	594	2	I58386
19	606	1.5	606	2	T11909
20	607	1.5	607	2	T13750
21	694	1.5	694	2	A95866
22	743	1.5	743	2	E87386
23	761	1.5	761	2	T03719
24	787	1.5	787	2	S68699
25	920	1.5	920	2	T10052
26	1309	1.5	1309	1	T35484
27	1622	1.5	1622	2	UE0378
28	51	1.3	51	2	S64676
29	87	1.3	87	2	AB1232

30	101	1.3	89	2	A82718	30S ribosomal prot
31	101	1.3	101	2	C95992	hypothetical prote
32	108	1.3	108	1	S15436	ribosomal protein
33	105	1.3	105	2	T26680	hypothetical prote
34	111	1.3	111	1	R85512	ribosomal protein
35	116	1.3	116	2	E72509	probable non speci
36	124	1.3	124	2	D89895	conserved hypothet
37	126	1.3	126	2	AD1509	hypothetical prote
38	134	1.3	134	2	A40959	secretin precursor
39	135	1.3	135	2	C96944	hypothetical prote
40	135	1.3	135	2	S67924	spore-wall fungal
41	136	1.3	136	2	T15207	hypothetical prote
42	141	1.3	141	2	G83312	probable type II ;
43	142	1.3	142	2	A89836	hypothetical prote
44	155	1.3	155	2	D83098	conserved hypothet
45	155	1.3	155	2	C83132	hypothetical prote
46	157	1.3	157	2	D31327	IgE receptor alpha
47	161	1.3	161	2	JC4728	mob protein B - Er
48	166	1.3	166	2	T49489	related to H-tran
49	175	1.3	175	2	E72262	conserved hypothet
50	178	1.3	178	2	B71824	hypothetical prote
51	181	1.3	181	2	B84121	hypothetical prote
52	182	1.3	182	2	JC7236	receptor-activity-
53	185	1.3	185	2	S76991	hypothetical prote
54	189	1.3	189	2	JC7262	receptor activity
55	197	1.3	197	2	H81007	phosphoprotein iso
56	202	1.3	202	2	A48486	orfX in mob region
57	202	1.3	202	2	C70650	hypothetical prote
58	209	1.3	209	2	H83133	hypothetical prote
59	212	1.3	212	2	A25856	ubiquitin thiolest
60	223	1.3	223	2	JX0222	ubiquitin thiolest
61	234	1.3	234	2	F95952	probable membrane-
62	235	1.3	235	2	T38440	flit3 ligand - huma
63	240	1.3	240	2	A39842	insulin-like growt
64	242	1.3	242	2	C93888	hypothetical prote
65	244	1.3	244	2	T04700	hypothetical prote
66	245	1.3	245	2	A30154	IgE receptor alpha
67	245	1.3	245	2	T26680	hypothetical prote
68	247	1.3	247	2	G83705	hypothetical prote
69	250	1.3	250	2	A34342	IgE FC receptor al
70	251	1.3	251	2	T07187	probable COI intro
71	257	1.3	257	2	C69230	conserved hypothet
72	268	1.3	268	2	A13189	hypothetical prote
73	269	1.3	269	2	W75576	cochlamn synthase
74	273	1.3	273	2	T12793	hypothetical prote
75	279	1.3	279	2	T29455	hypothetical prote

ALIGNMENTS

RESULT 1
T08732
hypothetical protein DKFZp56B0846.1 - human (fragment)
C:Species: Homo sapiens (homo)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_Change 13-Aug-1999
C:Accession: T08732
R:Ostenweider, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, May 1999
A:Reference number: Z15474
A:Accession: T08732
A:Molecule type: mRNA
A:Residues: 1-407 <OT>
A:Cross-references: EMBL:AL050071
A:Experimental source: fetal kidney; clone DKFZp56B0846
C:Genetics:
A:Note: DKFZp56B0846.1

Query Match 58.7%, Score 322, DB 2, Length 407;
Best Local Similarity 100.0%, Pred. No. 1,7e-303;
Matches 322; Conservative 0; Mismatches 0; Gaps 0;
QY 143 SGRYICRAVTFPLGNASSTVTVLVEPTVSLIKGFDLIDGNETVNAICIAATGRPVA 202

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|||||
Db 1 SGYICKAVTFPLGNASSITVYLVPEPSLJKPDSJIDGNETVAICIAITGPPA 60
OY 203 HIMEDCDLCEMESTTSPNETATIIISQYLFPTFRAGRTICVVKPALEKDIRSFI 262
Db 61 HIMEDDGLCEMESTTSPNETATIIISQYLFPTFRAGRTICVVKPALEKDIRSFI 120
OY 263 LDIOYAPESVYTCYGNMFVGRKGVNLCNADANPPFRSVWSRLDQMPDGLASDNTL 322
Db 121 LDIOYAPESVYTCYGNMFVGRKGVNLCNADANPPFRSVWSRLDQMPDGLASDNTL 180
OY 323 HFVHPLTFNYSQYICKVTNSLQGRSDQKVIYISDPPTTTLQPTIQWHSTADIEDLAT 382
Db 181 HFVHPLTFNYSQYICKVTNSLQGRSDQKVIYISDPPTTTLQPTIQWHSTADIEDLAT 240
OY 383 EPKKLPPLSTLATIKDITNTITIASVVGALPIVYVSLAGITCYRRRRFGDVFAN 442
Db 241 EPKKLPPLSTLATIKDITNTITIASVVGALPIVYVSLAGITCYRRRRFGDVFAN 300
OY 443 YIPPSDMOKESQIDVLQODEID 464
Db 301 YIPPSDMOKESQIDVLQODEID 322

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RESULT 2

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H71133
hypothetical protein PH0836 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C:Accession: H71133
R:Kawabuchi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohnishi, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A71000; MUID:9834437
A:Accession: H71133
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-100 <KAN>
A:Cross-references: GB:AP000003; MID:93236130; PIDN:BA29930.1; PID:93257247
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by Genbank
C:Genetics:
A:Gene: PH0836
C:Superfamily: Pyrococcus horikoshii hypothetical protein PH0836

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Query Match 1.5%; Score 8; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 41 LLLFPLLL 48
Db 71 LLLFPLLL 78

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RESULT 3

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T06479
proline/leucine-rich protein precursor - garden pea
C:Species: Pisum sativum (garden pea)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-Nov-1999
C:Accession: T06479
R:Rodriguez-Concepcion, M.; Perez-Garcia, A.; Beitran, J.
Submitted to the EMBL data library, November 1995
A:Description: Isolation of cDNAs which accumulate during pea (Pisum sativum L.) early
A:Reference number: 215708
A:Accession: T06479
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-106 <ROD>
A:Cross-references: EMBL:267873; NID:91213129; PIDN:CAA91780.1; PID:6208986
C:Date: 17-Jan-1995 #sequence_revision 17-Jan-1995 #text_change 05-Nov-1999
C:Product: proline/leucine-rich protein #status predicted <MAN>

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Query Match 1.5%; Score 8; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 36 PPLLL 43
Db 79 PPLLL 86

```

RESULT 4

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A55410
Ig light chain V region (variant CA2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
C:Accession: A55410
R:Tachibana, H.; Kido, I.; Murakami, H.
J. Biol. Chem. 269, 29061-29066, 1994
A:Title: Heterogeneous expression of human antibody lambda chains by concanavalin A
A:Reference number: A55410; MUID:95050725
A:Accession: A55410
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <TAC>
A:Cross-references: GB:S74107
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMH>

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Query Match 1.5%; Score 8; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 41 LLLFPLLL 48
Db 6 LLLFPLLL 13

```

RESULT 5

```

G83178
conserved hypothetical protein PA3747 [imported] - Pseudomonas aeruginosa (strain PA
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: G83178
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.
adman, S.; Yuan, Y.; Brode, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lathig, K.;
Lory, S.; Olson, M.V.
Nature 406, 939-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic
A:Reference number: AB2950; MUID:20437337
A:Accession: G83178
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-266 <STO>
A:Cross-references: GB:AF004793; GB:AE004091; NID:99949904; PIDN:AA607134.1; GSPDB:G
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3747

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Query Match 1.5%; Score 8; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 39 LLLFPL 46
Db 92 LLLFPL 99

```

RESULT 6

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S47094
hypothetical protein - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47094

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OM protein - protein search, using sw model

Run on: November 4, 2002, 12:02:17 ; Search time 6.76126 seconds
(without alignments)
2021.309 Million cell updates/sec

Title: US-09-972-268-6_COPY_74_152
Perfect score: 416
Sequence: 1 VELKCLIEVNETTIOISWEK.....ITLHNIGFSDSGKYCKAVT 79

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP mhc: *
8: SP organelle: *
9: SP phage: *
10: SP plant: *
11: SP rodent: *
12: SP virus: *
13: SP vertebrate: *
14: SP unclassified: *
15: SP virus: *
16: SP dactariap: *
17: SP archaea: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	416	100.0	549	09N0S3	09N0S3 homo sapien
2	410	98.6	438	09J1B7	09J1B7 mus musculu
3	410	98.6	510	09J1B8	09J1B8 mus musculu
4	410	98.6	549	09D006	09D006 mus musculu
5	410	98.6	549	09J1B9	09J1B9 mus musculu
6	137	32.9	295	09G175	09G175 bos taurus
7	132	31.7	295	09G175	09G175 bos taurus
8	131.5	31.6	298	09G174	09G174 cercoptilhec
9	114.5	27.5	261	09D6A9	09D6A9 mus musculu
10	114.5	27.5	408	09J1W1	09J1W1 mus musculu
11	109.5	26.3	336	015762	015762 homo sapien
12	109.5	26.3	336	046551	046551 hylobates s
13	108.5	26.1	336	018906	018906 macaca mula
14	103	24.8	269	09A3J3	09A3J3 homo sapien
15	103	24.8	271	040948	040948 kaposi's sa
16	103	24.8	348	088963	088963 kaposi's sa

17	101.5	24.4	510	4	096N78	096N78 homo sapien
18	101.5	24.4	510	4	096K15	096K15 homo sapien
19	99	23.8	253	12	09NRM1	09NRM1 macaca mula
20	98.5	23.7	467	11	091VT9	091VT9 mus musculu
21	94	22.6	222	11	09J1D5	09J1D5 mus musculu
22	94	22.6	278	11	054816	054816 mus musculu
23	94	22.6	478	11	054901	054901 mus musculu
24	92.5	22.2	412	11	09J1E1	09J1E1 ratius norv
25	92.5	22.2	415	11	060977	060977 mus musculu
26	91.5	22.0	601	11	099M67	099M67 mus musculu
27	89.5	21.5	355	11	0921X7	0921X7 mus musculu
28	89.5	21.5	360	11	0921X9	0921X9 mus musculu
29	87.5	21.0	412	11	063611	063611 ratius norv
30	87.5	21.0	7962	4	010465	010465 homo sapien
31	85.5	20.6	449	4	09J1E6	09J1E6 homo sapien
32	85.5	20.6	479	4	096J29	096J29 homo sapien
33	83.5	20.1	259	4	095532	095532 homo sapien
34	82	19.7	417	4	096B01	096B01 homo sapien
35	82	19.7	1021	13	079757	079757 gallus galli
36	80	19.2	1379	13	079701	079701 coturnix co
37	78.5	18.9	120	12	09DHH2	09DHH2 yaba-like d
38	78.5	18.9	186	12	091NM6	091NM6 lumpy skin
39	78.5	18.9	483	11	09DBP8	09DBP8 mus musculu
40	77.5	18.6	138	13	09YHF7	09YHF7 ginglymosto
41	77.5	18.6	310	11	09EPK4	09EPK4 mus musculu
42	77	18.5	310	11	09DBR7	09DBR7 mus musculu
43	77	18.5	310	11	09DIM9	09DIM9 mus musculu
44	77	18.5	318	13	091664	091664 xenopus lae
45	77	18.5	407	11	09D2J4	09D2J4 mus musculu

ALIGNMENTS

RESULT 1

ID	09N0S3	PRELIMINARY:	PRT:	549 AA.
AC	09N0S3			
DT	01-OCT-2000 (TEMBLrel. 15, Created)			
DT	01-OCT-2000 (TEMBLrel. 15, Last sequence update)			
DT	01-DEC-2001 (TEMBLrel. 19, Last annotation update)			
DE	NECTIN 3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Reynold M., Borg J.-P., Lecocq E., Adelaide J., Campadelli-Fiume G.,			
RA	Dubreuil P., Lopez M.,			
RT	"Human nectin 3/PR3: A novel member of the PVR/PRR/nectin family that			
RT	interacts with afadin.",			
RL	Gene 0:0-0(2000).			
DR	EMBL: AF282874; AAF97597.1; -			
DR	InterPro: IPR003599; Ig_			
DR	InterPro: IPR003600; Ig_1ike.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	Pfam: PF00047; Ig_2.			
DR	SMART: SM00409; Ig_1.			
DR	SMART: SM00410; Ig_1ike; 1.			
SO	SEQUENCE 549 AA; 61002 MW; 601104CDBA49D731 CRC64;			
Query Match	100.0%;	Score 416;	DB 4;	Length 549;
Best Local Similarity	100.0%;	Pred. No. 1e-39;		
Matches 79;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Oy	1 VELKCLIEVNETTIOISWEKSSQTVAVHHPQYGSVOGEYGRVLFNNYSYNDATI 60			
Db	74 VELKCLIEVNETTIOISWEKSSQTVAVHHPQYGSVOGEYGRVLFNNYSYNDATI 133			
Oy	61 TLANTGFSDSGKYCKAVT 79			
Db	134 TLANTGFSDSGKYCKAVT 152			

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RESULT 2
09JLB7      PRELIMINARY; PRT: 438 AA.
ID 09JLB7;
AC 09JLB7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE CELL ADHESION MOLECULE NECTIN-3 GAMMA.
GN PVR13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20209403; PubMed-10744716;
RA Satoh-Horikawa K., Nakamishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
that shows homophilic and heterophilic cell-cell adhesion
activities."
RT J. Biol. Chem. 275:10291-10299(2000).
RL
DR EMBL; AF195835; AAF63687.1; -.
DR MGD; MGI:1930171; Pvr13.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00410; Ig_1.
DR NCBI_TaxID=10090;
SO SEQUENCE 438 AA; 47261 MW; 2A0A441E5802EE CRC64;

Query Match 98.6%; Score 410; DB 11; Length 438;
Best Local Similarity 97.5%; Pred. No. 3, 8e-39;
Matches 77; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSXKCLIEVNETIQTQISMERIKGKSSQTVAAVHHPOYGFSGVGEVGFVFNKYSINDATI 60
DB 74 VSXKCLIEVNETIQTQISMERIKGKSSQTVAAVHHPOYGFSGVGEVGFVFNKYSINDATI 133
OY 61 TLHNIGFSDSGKYICKAVT 79
DB 134 TLHNIGFSDSGKYICKAVT 152

RESULT 3
09JLB8      PRELIMINARY; PRT: 510 AA.
ID 09JLB8;
AC 09JLB8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE CELL ADHESION MOLECULE NECTIN-3 BETA.
GN PVR13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20209403; PubMed-10744716;
RA Satoh-Horikawa K., Nakamishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
that shows homophilic and heterophilic cell-cell adhesion
activities."
RT J. Biol. Chem. 275:10291-10299(2000).
RL
DR EMBL; AF195834; AAF63686.1; -.
DR MGD; MGI:1930171; Pvr13.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00410; Ig_1.
DR NCBI_TaxID=10090;
SO SEQUENCE 549 AA; 60703 MW; 32775C8EC7319B32 CRC64;

Query Match 98.6%; Score 410; DB 11; Length 549;
Best Local Similarity 97.5%; Pred. No. 5e-39;
Matches 77; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSXKCLIEVNETIQTQISMERIKGKSSQTVAAVHHPOYGFSGVGEVGFVFNKYSINDATI 60
DB 74 VSXKCLIEVNETIQTQISMERIKGKSSQTVAAVHHPOYGFSGVGEVGFVFNKYSINDATI 133

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DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; Ig_1.
DR SMART; SM00410; Ig_Like; 1.
SO SEQUENCE 510 AA; 55811 MW; 45CFE6EE78454864 CRC64;

Query Match 98.6%; Score 410; DB 11; Length 510;
Best Local Similarity 97.5%; Pred. No. 4, 6e-39;
Matches 77; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSXKCLIEVNETIQTQISMERIKGKSSQTVAAVHHPOYGFSGVGEVGFVFNKYSINDATI 60
DB 74 VSXKCLIEVNETIQTQISMERIKGKSSQTVAAVHHPOYGFSGVGEVGFVFNKYSINDATI 133
OY 61 TLHNIGFSDSGKYICKAVT 79
DB 134 TLHNIGFSDSGKYICKAVT 152

RESULT 4
09D006      PRELIMINARY; PRT: 549 AA.
ID 09D006;
AC 09D006;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE 2610301B19RIK PROTEIN.
GN 2610301B19RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=EMBRIO;
RX MEDLINE-21085660; PubMed-11217851;
RA Kawai J., Shimagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kodono K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Koehli H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Resole G., Quackenbush J.,
RA Schmitt L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsi G.,
RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guslinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakemoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilmink L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohitsuki S.,
RA Hayashitani Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RT Nature 405:685-690(2001).
RL
DR EMBL; AK011949; BAB27933.1; -.
DR MGD; MGI:1914402; 2610301B19RIK.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00410; Ig_1.
DR SMART; SM00410; Ig_Like; 1.
SO SEQUENCE 549 AA; 60703 MW; 32775C8EC7319B32 CRC64;

Query Match 98.6%; Score 410; DB 11; Length 549;
Best Local Similarity 97.5%; Pred. No. 5e-39;
Matches 77; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSXKCLIEVNETIQTQISMERIKGKSSQTVAAVHHPOYGFSGVGEVGFVFNKYSINDATI 60
DB 74 VSXKCLIEVNETIQTQISMERIKGKSSQTVAAVHHPOYGFSGVGEVGFVFNKYSINDATI 133

```

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 4, 2002, 13:13:17 ; Search time 21 Seconds
(without alignments)

2512.050 Million cell updates/sec

Title: US-09-972-268-6

Perfect score: 2901 1 MARTLRPSPLCRGGKQAQLS.....EDDLVSHVDGVSIRREMY 549

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0*

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2141	73.8	407	2 T08732	hypothetical prote
2	627	21.6	518	2 UC4024	poliovirus recepto
3	494	17.0	467	1 HLMP3	poliovirus recepto
4	470	16.2	530	2 A53437	poliovirus recepto
5	463.5	16.0	478	2 I53960	PRR2 alpha - human
6	449.5	15.5	538	2 I68093	PRR2 delta - human
7	442.5	14.6	417	2 A44194	poliovirus recepto
8	415.5	14.3	392	2 B44194	poliovirus recepto
9	390.5	13.5	392	1 RRMUPD	poliovirus recepto
10	390.5	13.5	417	1 RWHUPA	poliovirus recepto
11	331.5	11.4	416	2 A54017	solon carcinoma as
12	230.5	7.9	764	2 A49448	irregular chiasm as
13	216.5	7.5	4391	2 A38096	perlecan precursor
14	201	6.9	5175	2 T20992	hypothetical prote
15	201	6.9	5198	2 T43290	hemocentin precurs
16	198	6.8	588	2 JH0506	adhesion molecule
17	194	6.7	588	2 A45254	surface glycoprote
18	189	6.5	853	1 JUBONG	neural cell adhesi
19	187.5	6.5	274	2 A47639	OX-2 membrane glyc
20	187.5	6.5	7962	2 I38346	elastic titin - hu
21	185	6.4	3707	2 S18552	heparin sulfate pr
22	182	6.3	587	2 JH0464	DM-GRSP precursor
23	181.5	6.3	1896	2 T08851	Down syndrome cell
24	178.5	6.2	847	2 JH0371	B-cell adhesion pr
25	174	6.0	858	1 JHRTNC	neural cell adhesi
26	173.5	6.0	761	1 JHUNG	neural cell adhesi
27	173	6.0	637	2 B33785	myelin-associated
28	172	5.9	513	2 JCS289	SHP substrate-1 pr
29	171.5	5.9	822	2 B49151	fibroblast growth

30	171	5.9	458	2 S23969	cell-adhesion mole
31	171	5.9	582	1 BNR73S	myelin-associated
32	171	5.9	626	1 BNR73S	myelin-associated
33	171	5.9	1259	2 A43425	Bravo/Nr-CAM cell
34	169.5	5.8	1091	1 JUCHNL	myelin cell adhesi
35	169	5.8	626	1 A61084	myelin-associated
36	168	5.8	765	2 C42632	cell adhesion mole
37	168	5.8	812	2 B42632	cell adhesion mole
38	168	5.8	932	2 A42632	cell adhesion mole
39	166.5	5.7	822	2 S19947	fibroblast growth
40	166	5.7	739	2 JN0581	vascular cell adhe
41	165	5.7	725	1 JUNGNG	neural cell adhesi
42	165	5.7	1115	1 JUNGNG	neural cell adhesi
43	164.5	5.7	569	2 A46462	T cell activation
44	164	5.7	521	2 JC1508	biliary glycoprote
45	163	5.6	458	1 WMSR1	biliary glycoprote

ALIGNMENTS

RESULT 1
T08732
Hypothetical protein DKFZps566B0846.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence revision 11-Jun-1999 #text change 13-Aug-1999
C:Accession: T08732
R:Ostenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A:Reference number: 216474
A:Accession: T08732
A:Molecule type: mRNA
A:Residues: 1-407 <COT>
A:Cross-references: EMBL:AL050071
A:Experimental source: fetal kidney; clone DKFZps566B0846
C:Genetics:
A:Note: DKFZps566B0846.1

Query Match 73.8%; Score 2141; DB 2; Length 407;
Best Local Similarity 99.3%; Pred. No. 7e-147;
Matches 404; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	143	SGKTYCAVFPPIGNAGOSTTATVLEPTYSIKGPDULDGNETVAALCIAGTKRPA	202
DB	1	SGKTYCAVFPPIGNAGOSTTATVLEPTYSIKGPDULDGNETVAALCIAGTKRPA	60
QY	203	HIWEGDLGMESTTSPNETATIIISQYLFPTFRAGRRITCVKHPALEKDIRSFT	262
DB	61	HIDWEGDLGMESTTSPNETATIIISQYLFPTFRAGRRITCVKHPALEKDIRSFT	120
QY	263	LDIQAVEVSVTGDGMFVGRKGVNLCNADANPPFKSVWSRLDQMPDGLASDNTL	322
DB	121	LDIQAVEVSVTGDGMFVGRKGVNLCNADANPPFKSVWSRLDQMPDGLASDNTL	180
QY	323	HFVPLTFNNSVYICKTNSIGORSQKVIYSDBPTTTLQPTOMHSTADIDLAT	382
DB	181	HFVPLTFNNSVYICKTNSIGORSQKVIYSDBPTTTLQPTOMHSTADIDLAT	240
QY	383	EPKLPPLSTLATTIKDTIATIIASVAGALFVLVSVLAGICFYRRRTFGDYFARN	442
DB	241	EPKLPPLSTLATTIKDTIATIIASVAGALFVLVSVLAGICFYRRRTFGDYFARN	300
QY	443	YLPSPDQKQSQIDVLOQDELSYPSVKKNKPNPNLIRKDYLEPEPKTONNNENTN	502
DB	301	YLPSPDQKQSQIDVLOQDELSYPSVKKNKPNPNLIRKDYLEPEPKTONNNENTN	360
QY	503	RFERPMDIYEDLGMKRYSDRHDENEDOLVSHVDGVSIRREMY 549	
DB	361	RFERPMDIYEDLGMKRYSDRHDENEDOLVSHVDGVSIRREMY 407	
RESULT 2			
	JC4024		

Gencore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 4, 2002, 13:13:37 ; Search time 32 Seconds

(Without alignments)
2967.944 Million cell updates/sec

Title: US-09-972-268-6

Perfect score: 2901
Sequence: 1 MARTLRPSLPCGGSKAQLS.....EDLVSHVDSVISREMY 549

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56222 seqs, 17299429 residues

1 number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : 1: SP archaea:.*
2: SP bacteria:.*
3: SP fungi:.*
4: SP human:.*
5: SP_invertebrate:.*
6: SP_mammal:.*
7: SP_mhc:.*
8: SP_organella:.*
9: SP_phage:.*
10: SP_plant:.*
11: SP_rodent:.*
12: SP_virus:.*
13: SP Vertebrate:.*
14: SP_unclassified:.*
15: SP_Virus:.*
16: SP_bacteriap:.*
17: SP_archaeap:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2901	100.0	549	4 Q9NOS3	Q9NOS3 homo sapien
2	2721	93.8	549	11 Q9JLB9	Q9JLB9 mus musculu
3	2677	92.3	549	11 Q9D006	Q9D006 mus musculu
4	2141	73.8	407	4 Q9Y412	Q9Y412 homo sapien
5	1814.5	62.5	510	11 Q9JLB8	Q9JLB8 mus musculu
6	1809.5	62.4	438	11 Q9JLB7	Q9JLB7 mus musculu
7	1639	56.2	304	4 Q9EVA9	Q9EVA9 mus sapien
8	544	18.8	510	4 Q9EVA8	Q9EVA8 mus sapien
9	543	18.7	510	4 Q9EVA7	Q9EVA7 mus sapien
10	534.5	18.4	295	11 Q9EVA5	Q9EVA5 mus sapien
11	528	18.2	298	6 Q9GL74	Q9GL74 cercoptilhec
12	526.5	18.1	295	6 Q9GL75	Q9GL75 bos taurus
13	496	17.1	99	11 Q9CTB0	Q9CTB0 mus musculu
14	494	17.0	467	11 Q9JLV8	Q9JLV8 mus musculu
15	493.5	17.0	483	11 Q9DBB8	Q9DBB8 mus musculu
16	463	16.0	479	4 Q96J29	Q96J29 homo sapien

17	432	14.9	449	4 Q9UE16	Q9UE16 homo sapien
18	413.5	14.3	412	11 Q9RE11	Q9RE11 ratius norv
19	408.5	14.1	412	11 Q63611	Q63611 ratius norv
20	400.5	13.8	401	6 Q08835	Q08835 cercoptilhec
21	393	13.5	408	11 Q9JWP1	Q9JWP1 mus musculu
22	390.5	13.5	417	4 Q96B21	Q96B21 homo sapien
23	346	11.9	415	11 Q60977	Q60977 mus musculu
24	337	11.6	494	11 Q9CRY3	Q9CRY3 mus musculu
25	334.5	11.5	442	4 Q9B6E7	Q9B6E7 homo sapien
26	271.5	9.4	336	11 Q9D6A9	Q9D6A9 mus musculu
27	250	8.6	261	11 Q9D6A9	Q9D6A9 mus musculu
28	247	8.5	396	11 Q9N928	Q9N928 mus musculu
29	234	8.1	959	5 Q9N919	Q9N919 drosophila
30	234	8.1	968	5 Q9W4T9	Q9W4T9 drosophila
31	233	8.0	306	11 Q9QTL4	Q9QTL4 mus musculu
32	233	8.0	432	4 Q9JUP1	Q9JUP1 homo sapien
33	229.5	7.9	975	5 Q97174	Q97174 drosophila
34	226.5	7.8	295	11 Q9QYL6	Q9QYL6 mus musculu
35	226.5	7.8	295	11 Q9Z2H8	Q9Z2H8 mus musculu
36	218	7.5	278	11 Q9QYL3	Q9QYL3 mus musculu
37	216.5	7.4	4370	4 Q9H3V5	Q9H3V5 homo sapien
38	215	7.4	345	5 Q9W4U1	Q9W4U1 drosophila
39	212.5	7.3	289	11 Q9QTL5	Q9QTL5 mus musculu
40	208	7.2	509	11 Q9QRL5	Q9QRL5 ratius norv
41	207	7.1	509	11 P97710	P97710 ratius norv
42	202	7.0	336	6 Q46551	Q46551 hyllobates s
43	202	7.0	5636	4 Q96RW7	Q96RW7 homo sapien
44	201	6.9	5198	5 Q76518	Q76518 caenorhabd1
45	200	6.9	336	6 Q18906	Q18906 macaca mula

ALIGNMENTS

RESULT 1	ID	Q9NOS3	PRELIMINARY:	PRT:	549 AA.
AC	Q9NOS3	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	NECTRIN 3				
OS	Homo sapiens (human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Reynold N., Borg J.-P., Lecocq E., Adelaide J., Campedel J., Fiume G.,				
RA	Dubreuil P., Lopez M.;				
RT	*Human nectin 3/PR3: A novel member of the PVR/PRR/nectin family that				
RT	interacts with afadin."				
RL	Gene 0.0-0(2000).				
DR	EMBL; AF282874; AAF97597.1; -				
DR	InterPro; IPR003599; Ig_				
DR	InterPro; IPR003600; Ig_Like.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	Pfam; PF00047; Ig_2.				
DR	SMART; SM00409; Ig_1.				
DR	SMART; SM00410; IG_Like; 1.				
SO	SEQUENCE 549 AA; 61002 MW; 6D1104CGBAA9D731 CRC64;				
Query Match	100.0%; Score 2901; DB 4; Length 549;				
Best Local Similarity	100.0%; Pred. No. 7,7e-221;				
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1 MARTLRPSLPCGGSKAQLSASLIGAGLLQPTPEPLLLFLFLFSRLCSALAGPI 60				
Db	1 MARTLRPSLPCGGSKAQLSASLIGAGLLQPTPEPLLLFLFLFSRLCSALAGPI 60				
Qy	61 IYEPHTVAVKGNVSKLILEVNETITQISKEITHGSSQYAVVHHPOYGSVGGEGGR 120				
Db	61 IYEPHTVAVKGNVSKLILEVNETITQISKEITHGSSQYAVVHHPOYGSVGGEGGR 120				

```

OY 121 VLEKNSLNDATITLHNGFSDSGKYICKAVTFPLGNAOSSTTVTVLVEPTVSLIKGPOS 180
DB 121 VLEKNSLNDATITLHNGFSDSGKYICKAVTFPLGNAOSSTTVTVLVEPTVSLIKGPOS 180
OY 181 LIDGNETVAALICATGKPAVHIDWEGDGLGEMESTTTSFNETATIIISQYKLEPFRAR 240
DB 181 LIDGNETVAALICATGKPAVHIDWEGDGLGEMESTTTSFNETATIIISQYKLEPFRAR 240
OY 241 GRRITCVVHPALEKDIRSFLLDIQYAPEVSVTGDNMFVGRKGVNLKCNADANPPF 300
DB 241 GRRITCVVHPALEKDIRSFLLDIQYAPEVSVTGDNMFVGRKGVNLKCNADANPPF 300
OY 301 KSVWSRLDQWPDGLASDNTLHFVHPLTFNYSGVYICKVNSLQORSQKVIYISDPPT 360
DB 301 KSVWSRLDQWPDGLASDNTLHFVHPLTFNYSGVYICKVNSLQORSQKVIYISDPPT 360
OY 361 TTTLOPTIQWHPSTADIEDLATEPKKLPPFLSTLATIKDDTITATIIASVYGALFLTVLS 420
DB 361 TTTLOPTIQWHPSTADIEDLATEPKKLPPFLSTLATIKDDTITATIIASVYGALFLTVLS 420
OY 421 VLACIFCYRRRTFRGDFPAKNYIPPSDMOKESQIDVLOQDELDSYPSVYKKNKPNVN 480
DB 421 VLACIFCYRRRTFRGDFPAKNYIPPSDMOKESQIDVLOQDELDSYPSVYKKNKPNVN 480
OY 481 LIRKDYLEPEKTOAWNENLNFRERPMOYEDLKMGMKFVSDHEHEDDLVSHVDS 540
DB 481 LIRKDYLEPEKTOAWNENLNFRERPMOYEDLKMGMKFVSDHEHEDDLVSHVDS 540
OY 541 VISREMYV 549
DB 541 VISREMYV 549

```

RESULT 2

09JLB9 PRELIMINARY: PRT: 549 AA.

AC 09JLB9: 01-OCT-2000 (TREMblrel. 15, Created)

DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE CELL ADHESION MOLECULE NECTIN-3 ALPHA.

GN PVR3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

EN [1]

SEQUENCE FROM N.A.

RA MEDLINE-20209403; PubMed-10744716;

RA Satoh-Horikawa K., Nakashishi H., Takahashi K., Miyahara M.,

RA Tachibana K., Mizoguchi A., Takai Y.;

RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules

RT that shows homophilic and heterophilic cell-cell adhesion

RT activities.";

RL J. Biol. Chem. 275:10291-10299(2000).

DR EMBL: AF195813; AAF63685.1; -.

DR MGD: MGI:1930171; Pvr3.

DR InterPro: IPR003599; Ig_.

DR InterPro: IPR003600; Ig_1like.

DR InterPro: IPR003006; Ig_MHC.

DR Pfam: PF00047; Ig_2.

DR SMART: SM00409; Ig_1.

DR SMART: SM00410; Ig_1like; 1.

SO SEQUENCE 549 AA: 60583 MW: 54929AB472P185 CRC64:

Query Match 93.88: Score 2721: DB 11: Length 549:

Best Local Similarity 92.98: Pred. No. 1.3e-206:

Matches 510: Conservative 19: Mismatches 20: Indels 0: Gaps 0:

MARTLRSPLCGGGKAQSSASLLGALLQPTPTPLLLPLPLLSRLCGALAGPT 60

CPAPLCGGGKAQSSASPPAAGLLPAPTPPLLLPLPLLSRLCGALAGST 60

```

OY 61 IVEPHVAVGKSNVSLKCLIEVNETITQISWEKIHKSSQCVAVHHPQCFGSYQGYQR 120
DB 61 IVEPHVAVGKSNVSLKCLIEVNETITQISWEKIHKSTQVAVHHPQCFGSYQGYQR 120
OY 121 VLEKNSLNDATITLHNGFSDSGKYICKAVTFPLGNAOSSTTVTVLVEPTVSLIKGPOS 180
DB 121 VLEKNSLNDATITLHNGFSDSGKYICKAVTFPLGNAOSSTTVTVLVEPTVSLIKGPOS 180
OY 181 LIDGNETVAALICATGKPAVHIDWEGDGLGEMESTTTSFNETATIIISQYKLEPFRAR 240
DB 181 LIDGNETVAALICATGKPAVHIDWEGDGLGEMESTTTSFNETATIIISQYKLEPFRAR 240
OY 241 GRRITCVVHPALEKDIRSFLLDIQYAPEVSVTGDNMFVGRKGVNLKCNADANPPF 300
DB 241 GRRITCVVHPALEKDIRSFLLDIQYAPEVSVTGDNMFVGRKGVNLKCNADANPPF 300
OY 301 KSVWSRLDQWPDGLASDNTLHFVHPLTFNYSGVYICKVNSLQORSQKVIYISDPPT 360
DB 301 KSVWSRLDQWPDGLASDNTLHFVHPLTFNYSGVYICKVNSLQORSQKVIYISDPPT 360
OY 361 TTTLOPTIQWHPSTADIEDLATEPKKLPPFLSTLATIKDDTITATIIASVYGALFLTVLS 420
DB 361 TTTLOPTIQWHPSTADIEDLATEPKKLPPFLSTLATIKDDTITATIIASVYGALFLTVLS 420
OY 421 VLACIFCYRRRTFRGDFPAKNYIPPSDMOKESQIDVLOQDELDSYPSVYKKNKPNVN 480
DB 421 VLACIFCYRRRTFRGDFPAKNYIPPSDMOKESQIDVLOQDELDSYPSVYKKNKPNVN 480
OY 481 LIRKDYLEPEKTOAWNENLNFRERPMOYEDLKMGMKFVSDHEHEDDLVSHVDS 540
DB 481 LIRKDYLEPEKTOAWNENLNFRERPMOYEDLKMGMKFVSDHEHEDDLVSHVDS 540
OY 541 VISREMYV 549
DB 541 VISREMYV 549

```

RESULT 3

09J006 PRELIMINARY: PRT: 549 AA.

AC 09J006: 01-JUN-2001 (TREMblrel. 17, Created)

DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE 2610301B19R1X PROTEIN.

GN 2610301B19R1X.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

EN [1]

SEQUENCE FROM N.A.

RA STRAIN-C57BL/6J; TISSUE-EMBRYO;

RA MEDLINE-21085660; PubMed-11217851;

RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,

RA Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana H.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasuwa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., Kling B., Kochiya H.,

RA Knehl P., Lewis S., Matsuo Y., Mikaldo I., Pesole G., Quackenbush J.,

RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Bottelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bolt C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Matzarelli U., Komdaers P.,

RA Noroche P., Ring B., Ringwald K., Rodriguez I., Sakamoto K.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Wittaker C., Wilming L.,

RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,

RA Hayashizaki Y.;